

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/039,177CDATE: 04/01/2001
TIME: 07:37:03

INPUT SET: S36583.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

pg 2,4

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Kohei MIYAZONO; Takeshe IMAMURA; Peter DEN DIJKE

(ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING
IT, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 46

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fulbright & Jaworski L.L.P.

(B) STREET: 666 Fifth Avenue

(C) CITY: New York City

(D) STATE: New York

(E) COUNTRY: USA

(F) ZIP: 10103

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb

(B) COMPUTER: IBM PS/2

(C) OPERATING SYSTEM: PC-DOS

(D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/039,177

(B) FILING DATE: March 13, 1998

(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/GB93/02367

(B) FILING DATE: November 17, 1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9224057.1

(B) FILING DATE: November 17, 1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9304677.9

(B) FILING DATE: March 8, 1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9304680.3

(B) FILING DATE: March 8, 1993

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/039,177CDATE: 04/01/2001
TIME: 07:37:03

INPUT SET: S36583.raw

46
47 (vii) PRIOR APPLICATION DATA:
48 (A) APPLICATION NUMBER: 9311047.6
49 (B) FILING DATE: May 28, 1993
50
51 (vii) PRIOR APPLICATION DATA:
52 (A) APPLICATION NUMBER: 9313763.6
53 (B) FILING DATE: July 2, 1993
54
55 (vii) PRIOR APPLICATION DATA:
56 (A) APPLICATION NUMBER: 9136099.2
57 (B) FILING DATE: August 3, 1993
58
59 (vii) PRIOR APPLICATION DATA:
60 (A) APPLICATION NUMBER: 321344.5
61 (B) FILING DATE: October 15, 1993
62
63 (viii) ATTORNEY/AGENT INFORMATION:
64 (A) NAME: Mary Anne Schofield
65 (B) REGISTRATION NUMBER: 36,669
66 (C) REFERENCE/DOCKET NUMBER: LUD 5539 CIP - JEL/MAS
67
68 (ix) TELECOMMUNICATION INFORMATION:
69 (A) TELEPHONE: (202) 662-0200
70 (B) TELEFAX: (202) 662-4643
71
72
73

ERRORED SEQUENCES FOLLOW:

2717 (2) INFORMATION FOR SEQ ID NO: 34:
2718 (i) SEQUENCE CHARACTERISTICS:
2719 (A) LENGTH: 513 amino acids
--> 2720 (B) TYPE: amino acid → format error: delete "7"
2721 (D) TOPOLOGY: linear
2722
2723 (ii) MOLECULE TYPE: peptide
2724
2725 (vi) ORIGINAL SOURCE:
2726 (A) ORGANISM: MOUSE
2727
2728 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
2729
2730
2731 Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
2732 5 10 15
2733 Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
2734 20 25 30
2735 Phe Asn Ala Asn Trp Glu lys Asp Arg Thr Asn Gln Thr Gly Val Glu

RAW SEQUENCE LISTING PATENT APPLICATION US/09/039,177C

DATE: 04/01/2001
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2736		35		40		45											
2737	Pro	Cys	Tyr	Gly	Asp	Lys	Asp	Lys	Arg	Arg	His	Cys	Phe	Ala	Thr	Trp	
2738		50					55					60					
2739	Lys	Asn	Ile	Ser	Gly	Ser	Ile	Glu	Ile	Val	Lys	Gln	Gly	Cys	Trp	Leu	
2740	65					70					75				80		
2741	Asp	Asp	Ile	Asn	Cys	Tyr	Asp	Arg	Thr	Asp	Cys	Val	Glu	Lys	Lys	Asp	
2742					85					90					95		
2743	Ser	Pro	Glu	Val	Tyr	Phe	Cys	Cys	Cys	Glu	Gly	Asn	Met	Cys	Asn	Glu	
2744				100					105					110			
2745	Lys	Phe	Ser	Tyr	Phe	Pro	Glu	Met	Glu	Val	Thr	Gln	Pro	Thr	Ser	Asn	
2746			115					120					125				
2747	Pro	Val	Thr	Pro	Lys	Pro	Pro	Tyr	Tyr	Asn	Ile	Leu	Leu	Tyr	Ser	Leu	
2748		130					135					140					
2749	Val	Pro	Leu	Met	Leu	Ile	Ala	Gly	Ile	Val	Ile	Cys	Ala	Phe	Trp	Val	
2750	145					150					155					160	
2751	Tyr	Arg	His	His	Lys	Met	Ala	Tyr	Pro	Pro	Val	Leu	Val	Pro	Thr	Gln	
2752					165					170						175	
2753	Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu	Leu	Gly	Leu	Lys	Pro	Leu	
2754				180					185					190			
2755	Gln	Leu	Leu	Glu	Val	Lys	Ala	Arg	Gly	Arg	Phe	Gly	Cys	Val	Trp	Lys	
2756			195				200					205					
2757	Ala	Gln	Leu	Leu	Asn	Glu	Tyr	Val	Ala	Val	Lys	Ile	Phe	Pro	Ile	Gln	
2758		210					215					220					
2759	Asp	Lys	Gln	Ser	Trp	Gln	Asn	Glu	Tyr	Glu	Val	Tyr	Ser	Leu	Pro	Gly	
2760	225					230				235						240	
2761	Met	Lys	His	Glu	Asn	Ile	Leu	Gln	Phe	Ile	Gly	Ala	Glu	Lys	Arg	Gly	
2762					245					250					255		
2763	Thr	Ser	Val	Asp	Val	Asp	Leu	Trp	Leu	Ile	Thr	Ala	Phe	His	Glu	Lys	
2764			260						265					270			
2765	Gly	Ser	Leu	Ser	Asp	Phe	Leu	Lys	Ala	Asn	Val	Val	Ser	Trp	Asn	Glu	
2766			275				280					285					
2767	Leu	Cys	His	Ile	Ala	Glu	Thr	Met	Ala	Arg	Gly	Leu	Ala	Tyr	Leu	His	
2768		290					295					300					
2769	Glu	Asp	Ile	Pro	Gly	Leu	Lys	Asp	Gly	His	Lys	Pro	Ala	Ile	Ser	His	
2770	305					310					315					320	
2771	Arg	Asp	Ile	Lys	Ser	Lys	Asn	Val	Leu	Leu	Lys	Asn	Asn	Leu	Thr	Ala	
2772					325					330					335		
2773	Cys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Leu	Lys	Phe	Glu	Ala	Gly	Lys	Ser	
2774			340						345					350			
2775	Ala	Gly	Asp	Thr	His	Gly	Gln	Val	Gly	Thr	Arg	Arg	Tyr	Met	Ala	Pro	
2776		355					360					365					
2777	Glu	Val	Leu	Glu	Gly	Ala	Ile	Asn	Phe	Gln	Arg	Asp	Ala	Phe	Leu	Arg	
2778		370					375					380					
2779	Ile	Asp	Met	Tyr	Ala	Met	Gly	Leu	Val	Leu	Trp	Glu	Leu	Ala	Ser	Arg	
2780	385					390					395					400	
2781	Cys	Thr	Ala	Ala	Asp	Gly	Pro	Val	Asp	Glu	Tyr	Met	Leu	Pro	Phe	Glu	
2782					405					410					415		
2783	Glu	Glu	Ile	Gly	Gln	His	Pro	Ser	Leu	Glu	Asp	Met	Gln	Glu	Val	Val	
2784			420						425					430			
2785	Val	His	Lys	Lys	Arg	Pro	Val	Leu	Arg	Asp	Tyr	Trp	Gln	Lys	His		
2786		435					440					445					
2787	Ala	Gly	Met	Ala	Met	Leu	Cys	Glu	Thr	Ile	Glu	Glu	Cys	Trp	Asp	His	
2788		450					455					460					

RAW SEQUENCE LISTING PATENT APPLICATION US/09/039,177C

DATE: 04/01/2001
TIME: 07:37:04

INPUT SET: S36583.raw

2789 Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
2790 465 470 475 480
2791 Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
2792 485 490 495
2793 Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
2794 500 505 510
2795 Leu
2796
2797

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2970 (2) INFORMATION FOR SEQ ID NO: 37:
2971 (i) SEQUENCE CHARACTERISTICS: *97 shown*
--> 2972 (A) LENGTH: 102 amino acids
--> 2973 (B) TYPE: amino acid *delete "7"*
2974 (D) TOPOLOGY: linear
2975
2976 (ii) MOLECULE TYPE: peptide
2977
2978 (vi) ORIGINAL SOURCE:
2979 (A) ORGANISM: C. elegans
2980
2981 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
2982
2983

*misaligned amino acid nos.
(see item 4 on Error Summary
sheet)*

2984 Cys His Cys Ser Arg Glu Val Gly Cys Asn Ala Arg Thr Thr Gly Trp
2985 5 10
2986 Val Pro Gly Ile Glu Phe Leu Asn Glu Thr Asp Arg Ser Phe Tyr Glu
2987 20 25 30
2988 Asn Thr Cys Tyr Thr Asp Gly Ser Cys Tyr Gln Ser Ala Arg Pro Ser
2989 35 40
2990 Pro Glu Ile Ser His Phe Gly Cys Met Asp Glu Lys Ser Val Thr Asp
2991 50 55 60
2992 Glu Thr Glu Phe His Asp Thr Ala Ala Lys Val Cys Thr Asn Asn Thr
2993 65 70
2994 Lys Asp Pro His Ala Thr Val Trp Ile Cys Cys Asp Lys Gly Asn Phe
2995 85 90
2996 Cys
2997
2998
2999

3125 (2) INFORMATION FOR SEQ ID NO: 46:
3126 (i) SEQUENCE CHARACTERISTICS:
--> 3127 (A) LENGTH: ? amino acids
3128 (B) TYPE: amino acid
3129 (D) TOPOLOGY: linear
3130
3131 (ii) MOLECULE TYPE: peptide
3132
3133 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
3134
3135 Gly Thr Ala Arg Tyr Met
3136 5

mandatory response needed (6 shown)

misaligned number

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/039,177CDATE: 04/01/2001
TIME: 07:37:04*INPUT SET: S36583.raw*

Line	Error	Original Text
29	Wrong Classification	(C) CLASSIFICATION: 435
2720	Unknown or Misplaced Identifier	(B) TY7PE: amino acid
2972	Entered (102) and Calc. Seq. Length (97) differ	(A) LENGTH: 102 amino acids
2973	Unknown or Misplaced Identifier	(B) TY7PE: amino acid
3127	Length must be an Integer	(A) LENGTH: amino acids
3127	Entered (0) and Calc. Seq. Length (6) differ	(A) LENGTH: amino acids

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Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/039,177c

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | | |
|----|-------------------------------------|-------------------------------------|--|
| 1 | ____ | Wrapped Nucleics | The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 2 | ____ | Wrapped Aminos | The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". |
| 3 | ____ | Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. |
| 4 | <input checked="" type="checkbox"/> | Misaligned Amino Acid
Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers. |
| 5 | ____ | Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed. |
| 6 | ____ | Variable Length | Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing. |
| 7 | ____ | PatentIn ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences. |
| 8 | ____ | Skipped Sequences
(OLD RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9 | ____ | Skipped Sequences
(NEW RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 10 | ____ | Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 11 | ____ | Use of <213>Organism
(NEW RULES) | Sequence(s) ____ are missing this mandatory field or its response. |
| 12 | ____ | Use of <220>Feature
(NEW RULES) | Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) |
| 13 | ____ | PatentIn ver. 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
"file," resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk. |

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